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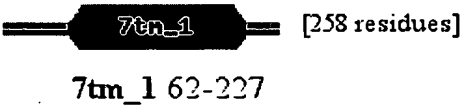
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FIGURE 1A

Domain	Start	End	Bits	Evalue	Alignment
7tm_1	62	227	142.90	2.6e-44	Align



Alignments of Pfam-A domains to HMMs

Format for fetching alignments to seed [Hypertext linked to swisspfam](#)

Alignment of 7tm_1 vs UserSeq/62-227

		*->GNILVilvilrtkkrlrtptnifiNLAvADLLflltlppwalyylvg	
		GN+LV +v++r+k +rt+tnifi++LA++DLL+++++ p++++ +	
UserSeq	62	GNALVFYVTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNIS	108
		gsedWpfGsalCklvtaldvvnmyaSi11LtaISiDRYlAIvhPlryrrr	
		+ W+ G + Ck v ++++++ + il++t+I++R++ vHP++ +	
UserSeq	109	--DNWLGGAFICKMVPFVQSTAVVTEILTMTCIAVERHQGLVHPFKMKWQ	156
		rtsprrrAkvvillvWvlalllslPp11fswvktveegngtln.vnvtvCl	
		+t rrA+ +++vW++a++++ P+ +++++ + + 1 +++++ Cl	
UserSeq	157	YT-NRRAFTMLGVVWLVAVIVGSPMWHVQOLEIKYDF---LYeKEHICCL	202
		idfpeestasvstwlrsyvllstlvGFllPl<-*	
		+ + ++ +++++y+++++++ FllPl	
UserSeq	203	EEWTSPV-----HQKIYTTFILVILFLLPL	227

FIGURE 1B

Model Seq-from Seq-to HMM-from HMM-to Score E-value Alignment				Description	
!! 7tm_1	62	332	1 275 211.7 8.2e-61	glocal 7 transmembrane receptor (rhodopsin family)	
<div></div>					
7tm_1 62-332					
7tm_1: domain 1 of 1, from 62 to 332: score 211.7, E = 8.2e-61					
*->GNLLVilvrlrtkklrtptnifilNLAVADLLfltlppwalyylvg					
GN+LV +v++r+k +rt+tnifi++LA++DLL+++++ p++++ +					
query	62	GNALVFYVWTRSKAMRTVTNIFICSLALSDLLITFFCIPVTMLQNIS			108
gsedWpGsalCklvtaldvvnmyasillLtaISiDRYLAIvhpIryrrr					
+ W+ G + Ck v +++++++ + il+++I+++R++ vhp++ +					
query	109	--DNWLGGAfICKMVPFVQSTAVVTEILTMTClAVERHQGLVHPFKMKWQ			156
rtsprrrAkvvillvWvLallslppllfswktveegngtln.vnvtvCl					
+t rRA+ ++++vW++a++++ P+ ++++ + + l +++++ Cl					
query	157	YT-NRRAFtMLGVVWLVAVIVGSPMWHVQQLKIKYDF--LYeKEHICCL			202
idfpeestasvstwlvsyvlstlvGfllPlvlvcytrIlrtlrkrar					
+ + ++ ++++++ FllPl v+l++Y+ I +l+ r					
query	203	EEWTSPV-----HQKIYtTfILVILfLLPLMVMlLYSKIGYELWIKKR			246
kgas.....kkrsskerkaaktllvvvvvFvLCWlPyfivllld					
g+ + ++ +++++ k ++k++++a +++++v +F++CW+P++++v ++					
query	247	VGdGsvlrlthgkemsKIARKKRRAVIMMVTVVAlFAVCWAPFHVVEHMI			296
tlc.lsiimsstCelervlptallvtl.wLayvNscInPiY<-*					
+ ++ e+ +v+ +++++++ +++++Ns+ NPi+Y					
query	297	EYSnFEK-----EYDDVTIKMIFAIVqIIGFSNSICNPiY			332

FIGURE 2

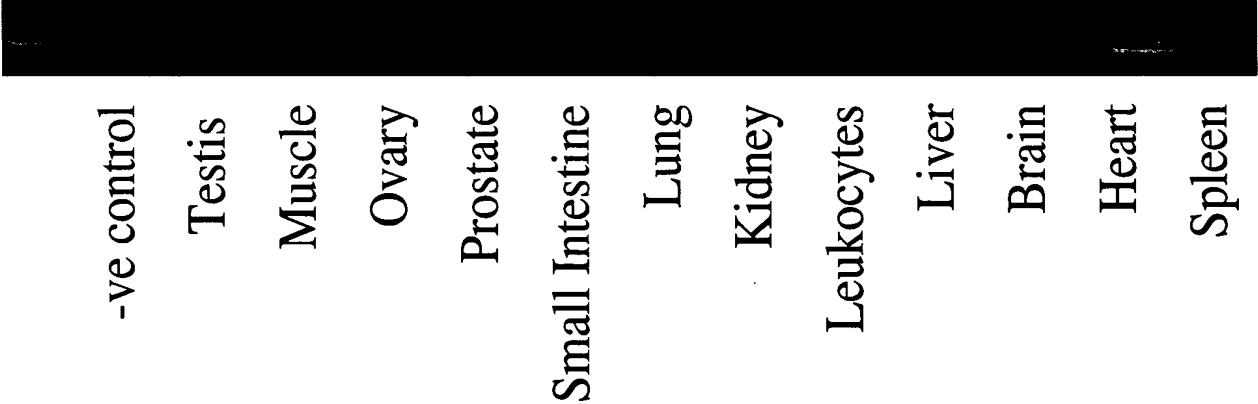


FIGURE 3

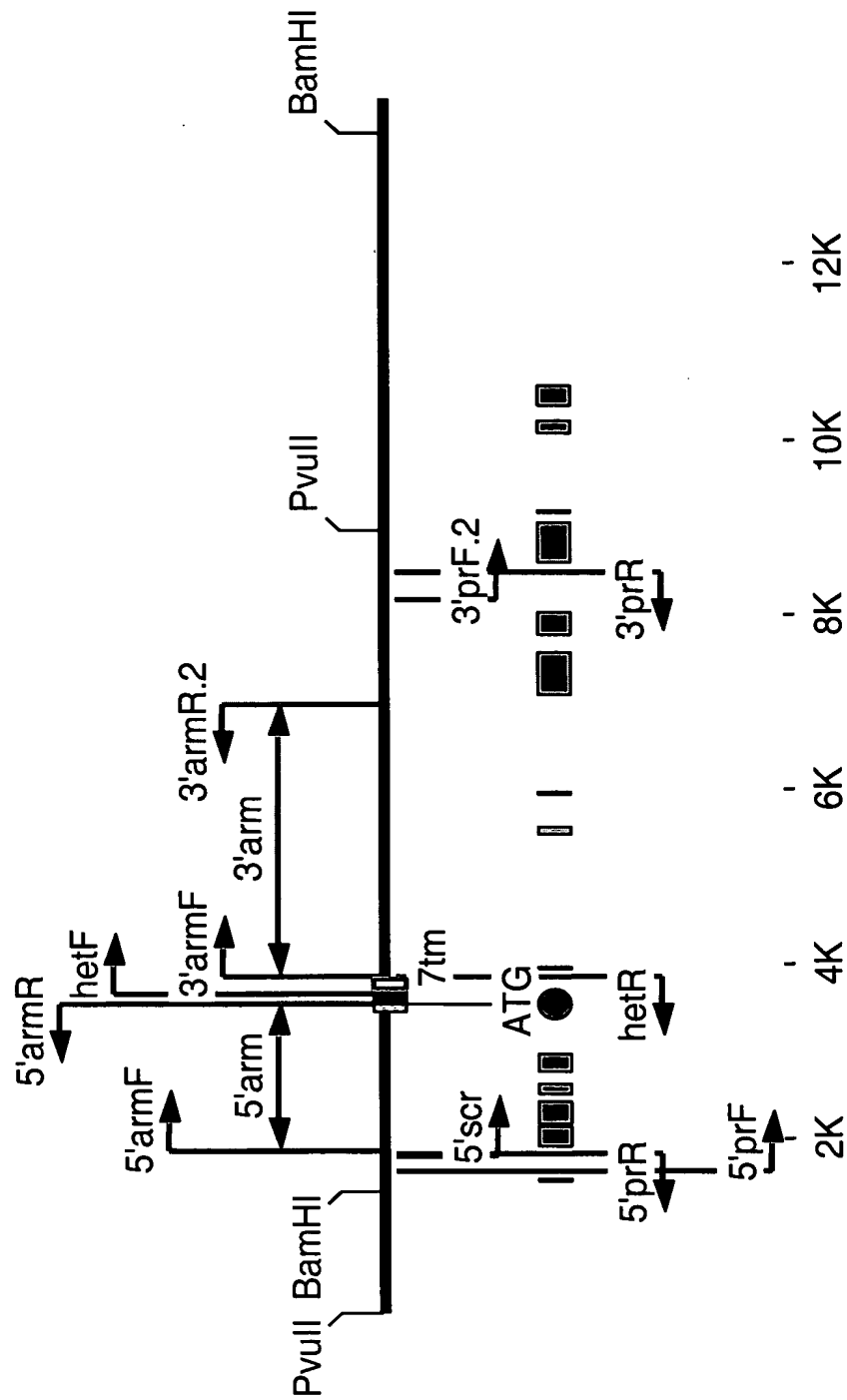


FIGURE 4

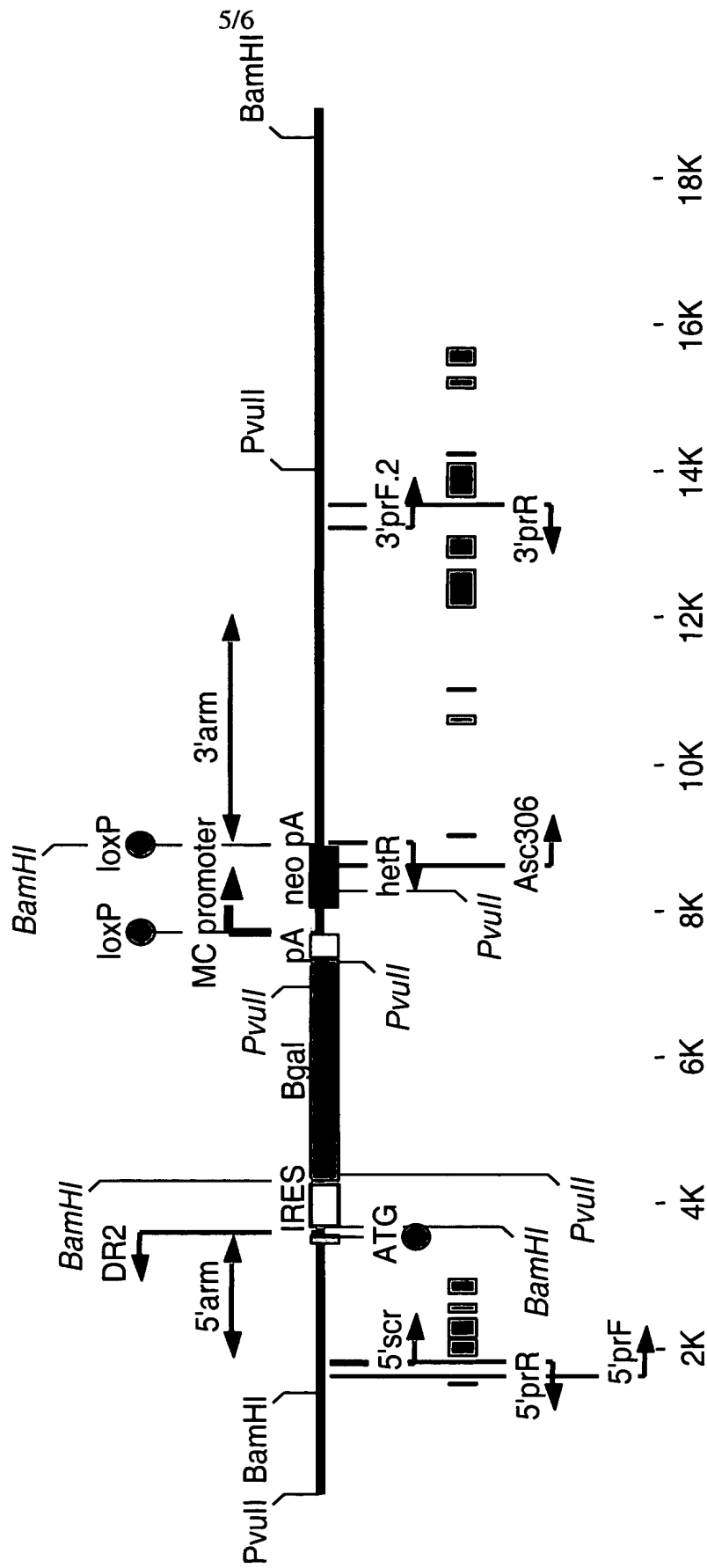


FIGURE 5

